

Circulating Fetuin-A and Risk of Type 2 Diabetes: A Mendelian Randomization Analysis

Janine Kröger (1,2), Karina Meidtner (1,2), Norbert Stefan (2,3,4), Marcela Guevara (5,6,7), Nicola D Kerrison (8), Eva Ardanaz (5,6,7), Dagfinn Aune (9,10), Heiner Boeing (11), Miren Dorronsoro (12,13,7), Courtney Dow (14,15,16), Guy Fagherazzi (14,15,16), Paul W Franks (17,18), Heinz Freisling (19), Marc J Gunter (19), José María Huerta (20,7), Rudolf Kaaks (21), Timothy J Key (22), Kay Tee Khaw (23), Vittorio Krogh (24), Tilman Kühn (25), Francesca Romana Mancini (14,26,16), Amalia Mattiello (27), Peter M Nilsson (17), Anja Olsen (28), Kim Overvad (29,30), Domenico Palli (31), J. Ramón Quirós (32), Olov Rolandsson (18), Carlotta Sacerdote (33,34), Núria Sala (35), Elena Salamanca-Fernández (36,37,7), Ivonne Sluijs (38), Annemieke MW Spijkerman (39), Anne Tjønneland (28), Konstantinos K Tsilidis (40,41), Rosario Tumino (42,43), Yvonne T van der Schouw (38), Nita G Forouhi (8), Stephen J Sharp (8), Claudia Langenberg (8), Elio Riboli (44), Matthias B Schulze (1,2), Nicholas J Wareham (8)

(1) Department of Molecular Epidemiology, German Institute of Human Nutrition Potsdam-Rehbruecke, Germany, (2) German Center for Diabetes Research (DZD), München-Neuherberg, Germany, (3) Department of Internal Medicine IV, University Hospital Tübingen, Tübingen, Germany, (4) Institute of Diabetes Research and Metabolic Diseases (IDM), Helmholtz Centre Munich at the University of Tübingen, Tübingen, Germany, (5) Navarre Public Health Institute (ISPN), Pamplona, Spain, (6) IdiSNA, Navarra Institute for Health Research, Pamplona, Spain, (7) CIBER de Epidemiología y Salud Pública (CIBERESP), Spain, (8) MRC Epidemiology Unit, University of Cambridge, Cambridge, United Kingdom, (9) Department of Epidemiology and Biostatistics, School of Public Health, Imperial College London, London, United Kingdom, (10) Bjørknes University College, Oslo,

Norway, (11) German Institute of Human Nutrition Potsdam-Rehbruecke, Germany, (12) Public Health Division of Gipuzkoa, San Sebastian, Spain, (13) Instituto BIO-Donostia, Basque Government, San Sebastian, Spain, (14) INSERM U1018, Center for Research in Epidemiology and Population Health, Villejuif, France, (15) Paris South-Paris Saclay University, Villejuif, France, (16) Gustave Roussy Institute, Villejuif, France, (17) Lund University, Malmö, Sweden, (18) Umeå University, Umeå, Sweden, (19) Section of Nutrition and Metabolism, International Agency for Research on Cancer (IARC-WHO), Lyon, France, (20) Department of Epidemiology, Murcia Regional Health Council, IMIB-Arrixaca, Murcia, Spain, (21) Division of Cancer Epidemiology, German Cancer Research Center (DKFZ), Heidelberg, Germany, (22) University of Oxford, United Kingdom, (23) University of Cambridge, Cambridge, UK, (24) Fondazione IRCCS Istituto Nazionale dei Tumori, Milano Italy, (25) German Cancer Research Centre (DKFZ), Heidelberg, Germany, (26) University Paris-Saclay, University Paris-Sud, Villejuif, France, (27) Dipartimento di Medicina Clinica e Chirurgia, Federico II University, Naples, Italy, (28) Danish Cancer Society Research Center, Copenhagen, Denmark, (29) Department of Public Health, Section for Epidemiology, Aarhus University, Aarhus, Denmark, (30) Aalborg University Hospital, Aalborg, Denmark, (31) Cancer Research and Prevention Institute (ISPO), Florence, Italy, (32) Public Health Directorate, Asturias, Spain, (33) Unit of Cancer Epidemiology, Citta' della Salute e della Scienza Hospital-University of Turin and Center for Cancer Prevention (CPO), Torino, Italy, (34) Human Genetics Foundation (HuGeF), Torino, Italy, (35) Unit of Nutrition and Cancer, Cancer Epidemiology Research Program, and Translational Research Laboratory, Catalan Institute of Oncology (IDIBELL), Barcelona, Spain, (36) Andalusian School of Public Health, Granada, Spain, (37) Instituto de Investigación Biosanitaria de Granada (Granada.ibs), Granada (Spain), (38) Julius Center for Health Sciences and Primary Care, University Medical Center Utrecht, Utrecht University, Utrecht, the Netherlands, (39) National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands, (40) Department

of Epidemiology and Biostatistics, School of Public Health, Imperial College London, London, UK, (41) Department of Hygiene and Epidemiology, University of Ioannina School of Medicine, Ioannina, Greece, (42) ASP Ragusa, Italy, (43) AIRE - ONLUS, Ragusa, Italy, (44) School of Public Health, Imperial College London, UK

Corresponding author:

Matthias B. Schulze, DrPH

German Institute of Human Nutrition Potsdam-Rehbruecke, Department of Molecular Epidemiology

Arthur-Scheunert-Allee 114-116, 14558 Nuthetal, Germany

Ph: +49 (0) 33200 88 2434

Fax: +49 (0) 33200 88 2437

Email: mschulze@dife.de

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ABSTRACT

Fetuin-A, a hepatic-origin protein, is strongly positively associated with risk of type 2 diabetes in human observational studies, but it is unknown whether this association is causal. We aimed to study the potential causal relation of circulating fetuin-A to risk of type 2 diabetes in a Mendelian Randomization study with SNPs located in the fetuin-A-encoding *AHSG* gene. We used data from eight European countries of the prospective EPIC-InterAct case-cohort study including 10,020 incident cases. Plasma fetuin-A concentration was measured in a subset of 965 subcohort participants and 654 cases. A genetic score of the *AHSG* SNPs was strongly associated with fetuin-A (28% explained variation). Using the genetic score as instrumental variable of fetuin-A, we observed no significant association of a 50 µg/ml higher fetuin-A concentration with diabetes risk (HR 1.02 [95%-CI 0.97, 1.07]). Combining our results with those from the Diabetes Genetics Replication And Meta-analysis (DIAGRAM) consortium (12,171 cases) also did not suggest a clear significant relation of fetuin-A with diabetes risk. In conclusion, although there is mechanistical evidence for an effect of fetuin-A on insulin sensitivity and secretion, this study doesn't support a strong, relevant relationship between circulating fetuin-A and diabetes risk in the general population.

Fetuin-A is a protein produced primarily by the liver, particularly in nonalcoholic fatty liver disease (1; 2). Fetuin-A is an inhibitor of the insulin receptor at the tyrosine kinase level (3; 4). Fetuin-A knockout mice were protected against insulin resistance (5; 6) and strong direct associations between fetuin-A levels and diabetes risk have been observed in prospective observational studies (7-13).

Fetuin-A is encoded by the *AHSG* gene. Earlier studies have shown strong associations of *AHSG* SNPs with fetuin-A levels (14; 15). The Mendelian Randomization approach, which involves the use of genetic information as an instrumental variable of the exposure, can be applied to estimate the potential causal effect of fetuin-A on diabetes risk (16). So far, only one small study has applied the Mendelian randomization approach to investigate fetuin-A in relation to risk of type 2 diabetes (17). This study suggested no causal involvement of fetuin-A (17), however, it was limited by low power to detect associations.

We therefore used data of the multicenter European Prospective Investigation into Cancer and Nutrition (EPIC)-InterAct study, with more than 10,000 incident cases of type 2 diabetes, to estimate the unconfounded effect of fetuin-A on diabetes risk with a Mendelian randomization approach. To maximize power, we additionally incorporated data from the Diabetes Genetics Replication And Meta-analysis (DIAGRAM) consortium involving further 12,171 type 2 diabetes cases.

RESEARCH DESIGN AND METHODS

EPIC-InterAct study

The EPIC-InterAct study is a case-cohort study nested within the prospective EPIC study (18). In brief, EPIC includes 519,978 men and women, mostly aged 35-70 years, who were recruited between 1991 and 2000 at 23 centers in ten European countries participating in EPIC (19). Each EPIC center obtained individual written informed consent and local ethics approval.

For the EPIC-InterAct study, incident cases of type 2 diabetes occurring in the EPIC cohort were ascertained and verified. All EPIC countries except Norway and Greece contributed to EPIC-InterAct ($n=455,680$). Individuals without stored blood ($n=109,625$) or without information on reported diabetes status ($n=5,821$) were excluded, leaving 340,234 participants eligible for inclusion in EPIC-InterAct (18).

Case-cohort construction and case ascertainment

A center-stratified, random subcohort of 16,835 individuals was selected. After exclusion of 548 individuals with prevalent diabetes and 133 with uncertain diabetes status, the subcohort included 16,154 individuals for analysis (18).

Details about the ascertainment of cases can be found in the supplemental material. Altogether, 12,403 verified incident cases were identified (18). In total, the EPIC-InterAct study involves 27,779 participants (16,154 subcohort members, 12,403 incident cases including 778 cases within the subcohort) (18).

Study Population for the Present Analysis

Figure 1 provides an overview of the study populations. As fetuin-A had been measured in Potsdam only, analyses involving fetuin-A were based on data of 1,593 participants from Potsdam (965 subcohort members, 654 incident cases including 26 cases within the

subcohort). Instrumental variable analysis was performed in the whole of EPIC-InterAct, excluding participants whose genetic data was not usable ($n=5,287$ due to insufficient amount of DNA, low call rate, X chromosome heterozygosity concordance with self-reported sex, outliers for heterozygosity, or lack of concordance with previous genotyping results) as well as EPIC-Potsdam participants with missing ($n=16$) or implausible ($n=97$) fetuin-A data, resulting in a dataset of 22,379 men and women (12,975 subcohort members, 10,020 incident cases). Analyses of the association of SNPs with potential confounders or mediators were performed after further exclusion of individuals ($n=3,946$) with missing values for these variables (dataset of 18,433 participants with 10,850 subcohort members and 8,108 cases).

Measurement of Fetuin-A and Other Biomarkers

Blood samples were taken at baseline. For the Potsdam participants, plasma levels of fetuin-A were measured in Tübingen, Germany, with the automatic ADVIA 1650 analyzer (Siemens Medical Solutions, Erlangen, Germany). An immunoturbidimetric method was used with specific polyclonal goat antihuman fetuin-A antibodies to human fetuin-A (BioVendor Laboratory Medicine, Modreci, Czech Republic). This method was evaluated in a side-by-side comparison with an ELISA (intra-assay CV: 3.5%, inter-assay: CV 5.4%, BioVendor) showing a correlation of $r=0.93$.

All other laboratory measures were done for all EPIC-InterAct participants by the Stichting Huisartsen Laboratorium Groep (Etten-Leur, the Netherlands, see Supplemental Material).

Genotyping, Identification of Tagging SNPs, and Construction of Genetic Scores

Details about genotyping methods can be found in the Supplemental material.

We selected five tagging SNPs of the *AHSG* gene (rs4917, rs2070635, rs2070633, rs2248690, rs4831) using HapMap 22/phaseII CEPH population data applying stringent criteria (minor allele frequency $>5\%$, pairwise $r^2 \geq 0.80$) as similarly done earlier (14). A genetic score was

created by summing the number of fetuin-A-raising alleles of the single SNPs. We also constructed a weighted genetic score to account for the different strength of association between SNPs and fetuin-A (details of instrumental variables described in the Supplemental Material).

Assessment of Other Covariables

Standardized questionnaires were used at baseline to collect information on sociodemographic characteristics and lifestyle including age, education level, smoking status, occupational and leisure-time physical activity, and history of previous illness. Height, weight, and waist circumference of participants were obtained by trained staff during the baseline examination using standardized protocols (20). However, for participants from France and some participants from Oxford (UK), self-reported anthropometric data were collected.

Statistical Analysis

The associations of SNPs with fetuin-A were determined by linear regression in the Potsdam subcohort with SNPs modeled per fetuin-A-increasing allele (additive model). First, the individual SNPs were analyzed in separate models. Then, all SNPs were included in the same model. SNPs showing a significant association with fetuin-A in this model were used to generate the genetic scores, with beta coefficients used as weights.

The associations of the genetic score with potential confounders or mediators were evaluated by linear regression for continuous and logistic regression for dichotomous confounders/mediators.

To study the association of genetic variables with diabetes, we performed Cox regression with Prentice weighting (21). Age was used as underlying time scale. Models were stratified by integers of age (years), study center, and genotyping source and further adjusted for sex. Heterogeneity between countries in the association of the genetic variables with diabetes risk

was investigated by computing country-specific hazard ratios and pooling these with random-effects meta-analyses.

We calculated instrumental variable estimates to estimate the unconfounded effect of an increase of 50µg/ml in fetuin-A on diabetes risk. We assumed very similar associations of *AHSG* SNPs and fetuin-A concentration between the Potsdam center and the other EPIC-InterAct centers and applied the two-stage least squares (2-SLS) procedure (22) for calculating instrumental variable estimates.

To increase power, we further included data from the DIAGRAM consortium (see Supplemental Material). Summary statistics were meta-analyzed with the OR and 95% CI of the respective SNP derived from EPIC-InterAct (after excluding the Norfolk center because this is included in DIAGRAM) using a fixed-effect model.

Statistical analyses were performed with SAS (version 9.4, Enterprise Guide 6.1; SAS Institute, Cary, NC, USA).

Furthermore, we performed a power calculation using the online tool mRnd (<http://glimmer.rstudio.com/kn3in/mRnd/>)(23), as described in the Supplemental Material.

RESULTS

Table 1 shows baseline characteristics for the subcohort members of the EPIC-InterAct study and of the Potsdam center.

Observational analysis of fetuin-A and diabetes risk

In EPIC-Potsdam, circulating fetuin-A was positively associated with diabetes, with a HR of 1.18 (95% CI: 1.05, 1.33) per 50 µg/ml in the multivariable-adjusted model (Supplemental Table 4). Additional adjustment for BMI and waist circumference did not alter the observed association.

Association of *AHSG* SNPs and genetic scores with fetuin-A and diabetes risk

In the Potsdam subcohort, four of the five *AHSG* SNPs were significantly associated with fetuin-A in univariate analyses (Supplemental Table 1). Including all five SNPs simultaneously in one model revealed significant associations for three SNPs (Table 2), which were subsequently used to create the genetic scores. Both the weighted (weighted by beta coefficients from linear regression) and the unweighted genetic score showed a strong association with fetuin-A explaining 28% and 27% of variation in fetuin-A, respectively. Both genetic scores were not associated with diabetes risk (Supplemental Figures 1, 2).

We detected no meaningful association of the weighted genetic score with potential confounders or mediators in the EPIC-InterAct subcohort (Supplemental Tables 2, 3).

Instrumental variable analysis of fetuin-A and diabetes

Using instrumental variable analysis to estimate the unconfounded association for a 50µg/ml higher fetuin-A level did not indicate an effect on diabetes risk in EPIC-InterAct. The HR for the weighted genetic score was 1.02 (95% CI 0.97, 1.07). Also for single SNPs, the HRs were generally very low in magnitude (between 1.01 and 1.04) and nonsignificant (Table 3). When

further combining EPIC-InterAct with DIAGRAM, the ORs for the single SNPs remained the same, but ORs for two SNPs became borderline significant (OR for rs4917=1.02 [95% CI 1.00, 1.06], OR for rs2248690=1.04 [95% CI 1.00, 1.08]).

We also analyzed potential differences in the association of the weighted genetic score with diabetes risk in EPIC-InterAct. Stratification by age, sex, waist circumference, or HbA_{1c} did not reveal meaningful differences between subgroups (Supplemental Table 4).

DISCUSSION

In this large European case-cohort study, instrumental variables reflecting circulating fetuin-A were not significantly associated with diabetes risk. Further meta-analyzing results with those from the DIAGRAM consortium to bolster statistical power also did not indicate a strong association of genetically-elevated fetuin-A with diabetes.

Several prospective observational studies have detected a significant and strong positive association between plasma fetuin-A levels and the risk of type 2 diabetes (7-13). We could not confirm this strong association in a Mendelian Randomization approach. Although we found borderline significant estimates for two SNPs (OR for rs4917=1.02 [95% CI 1.00, 1.06], OR for rs2248690=1.04 [95% CI 1.00, 1.08]), our results do not suggest a strong causal association because an allele increase corresponds to a high difference in fetuin-A (50µg/ml, SD for fetuin-A=61µg/ml). According to our results of the observational analysis, we would have expected an OR of 1.18. Due to the use of different assays to determine concentrations of fetuin-A across studies, we could not calculate expected ORs based on the other observational studies on fetuin-A and diabetes risk. the slightly stronger associations of *AHSG* SNPs with fetuin-a (17) than in EPIC-Potsdam and results of quantile comparisons (7-9; 11; 12) suggest even higher expected ORs based on these studies.

Our study was not designed to unravel specific factors that explain the results of earlier observational studies, but it suggests that fetuin-A concentration more strongly reflects an adverse metabolic profile than being an important causal risk factor in the pathogenesis of diabetes.

Our results are in agreement with those from an earlier small study on *AHSG* SNPs and diabetes risk involving older adults (17). Fetuin-A was positively associated with fasting

glucose levels, but *AHSG* SNPs did not support an association between genetically predicted fetuin-A concentrations and fasting glucose or diabetes risk. A major limitation of this study is the small study size resulting in a low power for the instrumental variable analysis (3,435 participants including 259 incident cases).

In experiments of mice and human adipocytes, it has been observed that free fatty acids (FFAs) require the presence of fetuin-A to induce an inflammatory signaling pathway resulting in insulin resistance and subclinical inflammation (24). Fetuin-A might indeed contribute to the development of type 2 diabetes in already predisposed individuals with high concentrations of FFAs. Supporting this assumption, an interaction of fetuin-A and FFAs in determining insulin sensitivity was observed in a study of 347 participants at increased risk for type 2 diabetes and CVD (25). In our study, the unavailability of FFA blood concentrations precluded us from investigating a potential effect modification by FFAs.

A major strength of our study relates to the large sample size for analyzing *AHSG* SNPs and genetic scores in relation to diabetes risk. *AHSG* SNPs and genetic scores showed strong associations with circulating fetuin-A resulting in powerful instrumental variables. All SNPs are located in the fetuin-A-encoding *AHSG* gene, making pleiotropic roles of the SNPs rather unlikely. As limitation, we have information on circulating fetuin-A only in the Potsdam center of EPIC-InterAct.

In conclusion, although there is mechanistical evidence for an effect of fetuin-A on insulin sensitivity and secretion, this study does not support a strong, relevant relationship between circulating fetuin-A and diabetes risk in the general population.

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Table 1 - Baseline characteristics of subcohort participants of the EPIC-InterAct study (n=10,850) and the Potsdam center (n=965)

	EPIC-InterAct	Potsdam center
<i>General characteristics</i>		
Age, years	53 (9)	50 (9)
Male	37	39
BMI (kg/m ²)	26.1 (4.2)	25.7 (4.1)
Current smoking	27	19
Physically active	21	16
Longer education	21	38
Alcohol intake (g/d)	7.4 (1.2, 20.1)	8.2 (3.1, 19.5)
<i>Biomarkers</i>		
Fetuin-A, µg/ml	-	267 (61)
GGT, U/l	20 (14, 32)	21 (15, 35)
ALT, U/l	18 (14, 25)	19 (14, 27)
Albumin, g/l	46 (3)	46 (3)
Creatinine, µmol/l	68 (60, 78)	69 (61, 80)
CRP, mg/l	1.1 (0.6, 2.4)	1.1 (0.6, 2.3)
HDL cholesterol, mmol/l	1.5 (0.4)	1.5 (0.4)
Total cholesterol, mmol/l	6.0 (1.1)	5.9 (1.1)
Triglycerides, mmol/l	1.1 (0.8, 1.7)	1.1 (0.8, 1.7)
HbA _{1c} , % (mmol/mol)	5.4 [5.2, 5.7] (36 [33, 39])	5.4 [5.1, 5.5] (35 [32, 37])
Values are mean (SD), median (interquartile range), or %		

Table 2 - Association of individual *AHSG* SNPs and genetic scores with fetuin-A concentration in the Potsdam part of the EPIC-InterAct study subcohort – Simultaneous adjustment of SNPs

	Allele	β (SE) for fetuin concentration	<i>p</i>	F statistic
<i>Individual SNPs</i>				
rs4917	T→C	16.9 (8.4)	0.0446	<0.0001
rs2070635	G→A	-0.6 (5.1)	0.9013	
rs2070633	T→C	23.7 (8.2)	0.0040	
rs2248690	T→A	12.3 (4.3)	0.0040	
rs4831	G→C	1.1 (8.6)	0.9008	
<i>Genetic scores*</i>				
Weighted score		52.4 (2.8)	<0.0001	<0.0001
Unweighted score		53.0 (2.8)	<0.0001	<0.0001
<i>n</i> =965				

β for individual SNPs obtained from one linear regression model including all five SNPs simultaneously, β for genetic scores obtained from single univariate linear regression models, SNPs and genetic scores modelled per fetuin-A-increasing allele and fetuin-A expressed in $\mu\text{g/ml}$

*Genetic scores were created as sum of fetuin-A-increasing alleles of rs4917, rs2070633 and rs2248690, divided by three. Betas of the three SNPs from linear regression have been used as weights for the weighted genetic score.

Table 3 - Instrumental variable estimates for the weighted genetic score and single *AHSG* SNPs reflecting the association of a 50µg/ml increase in fetuin-A concentration with diabetes risk

	Weighted genetic score	rs4917	rs2070633	rs2248690
EPIC-InterAct*	1.02 (0.97, 1.07)	1.02 (0.98, 1.07)	1.01 (0.95, 1.08)	1.04 (0.96, 1.10)
EPIC-InterAct and DIAGRAM combined†		1.02 (1.00, 1.06)	1.01 (0.98, 1.05)	1.04 (1.00, 1.08)

Data are HRs (for EPIC-InterAct) or ORs (for EPIC-InterAct and DIAGRAM combined) and 95% CIs per 50µg/ml increase in fetuin-A concentration. Instrumental variable estimates were obtained from two-stage least squares procedure. Estimates for EPIC-InterAct and DIAGRAM have been combined with a fixed-effects meta-analysis.

* $n=22,379$ including 12,975 incident cases of type 2 diabetes

† DIAGRAM: $n=69,033$ including 12,171 incident cases of type 2 diabetes

Figure 1 Construction of the EPIC-InterAct case-cohort study and the study populations used for the present analysis

ONLINE SUPPLEMENTAL MATERIALS

Case ascertainment

Ascertainment of incident type 2 diabetes involved a review of the existing EPIC datasets at each center using multiple sources of evidence including self-report, linkage to primary-care registers, secondary-care registers, medication use (drug registers), hospital admissions and mortality data. Information from any follow-up visit or external evidence with a date later than the baseline visit was used. Rather than self-report, cases in Denmark and Sweden were identified via local and national diabetes and pharmaceutical registers and hence all ascertained cases were considered to be verified. Some cases in centers other than Denmark and Sweden were based on only one source of information. To increase the specificity of the definition for these cases, we sought further evidence including review of individual medical records in some centers. Follow-up was censored at the date of diagnosis, 31 December 2007 or the date of death, whichever occurred first.

Measurement of biomarkers (except fetuin-A)

The measurements were performed on serum (except for participants in the Umeå center in Sweden, where only plasma samples were available) or erythrocyte samples that had been previously frozen in liquid nitrogen or at ultra-low-temperature freezers at -80°C (samples from Umea, Sweden). γ -glutamyltransferase (GGT), alanine transaminase (ALT), albumin, creatinine, C-reactive protein (CRP), high-density lipoprotein (HDL) cholesterol, total cholesterol, and triglycerides were measured using a Cobas[®] (Roche Diagnostics, Mannheim, Germany) assay on a Roche Hitachi Modular P analyzer. Erythrocyte HbA_{1c} was measured using Tosoh (HLC-723G8) ion exchange high-performance liquid chromatography on a Tosoh G8 analyzer.

Genotyping

DNA was extracted from buffy coat from a citrated blood sample using standard procedures on an automated Autopure LS DNA extraction system (Qiagen, Hilden, Germany) with PUREGENE chemistry (Qiagen). The DNA was hydrated overnight prior to further processing, quantified by PicoGreen assay (Quant-iT) and normalised to 50 ng/ μ l. Samples were genotyped if they had sufficient DNA, could be successfully genotyped on Taqman or Sequenom platforms and had sex chromosome genotypes concordant with self-reported sex. Samples that failed one genotyping round were repeated in another if they failed for reasons that may not relate to sample quality (e.g. signal intensity outliers or plates/arrays with an unusually high failure rate). Samples to be genotyped on the Illumina 660 W-Quad BeadChip were randomly selected from the available samples with the number of individuals selected per center being proportional to the percentage of total cases in that center. Danish samples were not available at this stage. Genotyping was carried out at the Wellcome Trust Sanger Institute. The remaining samples were genotyped on either the Illumina HumanCoreExome-12 or HumanCoreExome-24 at Cambridge Genomic Services in the University of Cambridge, Department of Pathology.

Before imputation, SNPs were filtered to remove those with minor allele count < 2 , call rate $< 95\%$ or Hardy Weinberg p-value $< 1e-6$. SNPs were also removed if they were not found in the Haplotype Reference Consortium (HRC) panel, were A/T or G/C with MAF > 0.4 , had an allele frequency difference > 0.2 with reference panel, or were indels. Imputation was performed at the Wellcome Trust Centre for Human Genetics using the HRC panel version 1.0 and IMPUTE v2.3.2 software.

Instrumental variable construction

Unless variants are highly correlated, all variants which can be reasonably assumed to be valid instruments can be included in a Mendelian randomization analysis to improve the precision of the causal estimate (1). To account for the high correlation within the AHSG gene, we first identified tagging SNPs based on HapMap 22/phaseII CEPH population data applying stringent criteria (minor allele frequency >5%, pairwise $r^2 \geq 0.80$) as similarly done earlier (2). As this selection process does not rule out high intercorrelation, the five SNPs identified (rs4917, rs2070635, rs2070633, rs2248690, rs4831) were subsequently included in the same regression model and gene scores as instrumental variables were based on those SNPs showing a significant independent association with fetuin-A in this model.

The recent GWAS by Jensen et al. (3) has identified several more SNPs to be univariately associated with fetuin-A levels. E.g. 5 SNPs showed very low p-values and were not in high LD with rs4917 in the GWAS (3). However, all 5 were well covered by rs2070633 (r^2 ranging from 0.811 to 0.875 based on HapMap CEPH) selected for our gene score. Overall, the considerable degree of LD among SNPs in the AHSG gene, the magnitude of association of other SNPs identified in the GWAS (3) besides those mentioned above (substantially weaker compared to rs4917), and the statistical power of our instrumental variables (see below) makes it unlikely that inclusion of additional SNPs would substantially improve our instrumental variable approach.

Meta-Analysis of DIAGRAM and EPIC-InterAct data

We have used summary statistics of a meta-analysis consisting of 12,171 type 2 diabetes cases and 56,862 controls across 12 GWAS as published elsewhere (4). All studies participating in DIAGRAM included men and women of European descent. DIAGRAM data are publicly

available at <http://diagram-consortium.org/downloads.html>. We extracted the odds ratio and corresponding 95% CIs for each of the three SNPs that were used to create the genetic scores (rs4917, rs2070633, rs2248690).

Power calculation

The power for the Mendelian Randomization analysis at a two-sided α of 0.05 was calculated based on the available sample size, the association of the genetic variables with fetuin-A concentration, and the expected causal effect estimate using the online tool mRnd (<http://glimmer.rstudio.com/kn3in/mRnd/>).

Given the HR of 1.18 per 50 $\mu\text{g/ml}$ higher fetuin-A in our observational analysis, we would have expected a HR of 1.19 per allele of the weighted genetic score based on the association of the genetic variables with fetuin-A concentration in the subcohort of the Potsdam center. In EPIC-InterAct, we have 99.9% power to detect this expected HR with the weighted genetic score or with the single SNPs (rs4917, rs2070633, and rs2248690). Combining our data with those from the DIAGRAM consortium further increased the power enabling us to detect a HR of 1.05 with sufficiently high power (89% power for rs4917, 89% for rs2070633, and 81% for rs2248690).

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Supplemental Table 1 - Association of individual AHSG SNPs with fetuin-A concentration in the Potsdam part of the EPIC-InterAct study subcohort

SNP	Allele	Allele	Mean level (µg/ml)			β (SE) for	<i>p</i>	<i>r</i> ²
	1	2	of fetuin-A			fetuin		
			by <i>AHSG</i> genotype			concentration		
			11	12	22			
rs4917	T	C	214	257	299	44.1 (2.6)	3.404573E-56	0.24
rs2070635	A	G	238	272	308	37.0 (2.6)	1.489007E-41	0.18
rs2070633	T	C	223	267	307	42.3 (2.5)	1.557487E-57	0.24
rs2248690	T	A	212	252	291	41.8 (2.9)	2.588671E-43	0.19
rs4831	G	C	270	267	272	4.0 (4.4)	0.3719	0.0009
<i>n</i> =965								

β obtained from single univariate linear regression models for each SNP with SNPs modelled per fetuin-A-increasing allele and fetuin-A expressed in µg/ml

Supplemental Table 2 - Association of weighted genetic score with potential confounders

Continuous traits	β (SE)	<i>p</i>
Age, years	-0.26 (0.13)	0.05
Alcohol intake, g/d	0.38 (0.30)	0.21
GGT, U/l	0.49 (0.63)	0.44
ALT, U/l	0.08 (0.21)	0.71
Albumin, g/l	-0.03 (0.05)	0.50
Creatinine, $\mu\text{mol/l}$	-0.17 (0.24)	0.49
Binary traits	Odds ratio (95% CI)	<i>p</i>
Sex, male	0.97 (0.91, 1.04)	0.41
Current smoking	0.93 (0.87, 1.00)	0.06
Physically active	1.01 (0.93, 1.09)	0.83
Longer education	0.94 (0.87, 1.02)	0.13
(incl. university)		

β obtained from linear regression (age, alcohol intake, GGT, ALT, albumin, creatinine) and ORs obtained from logistic regression (sex, current smoking, physically active, longer education); estimates are per fetuin-A-increasing allele of the weighted genetic score, adjusted for country among 10,850 subcohort participants

Supplemental Table 3 - Association of weighted genetic score with potential mediators

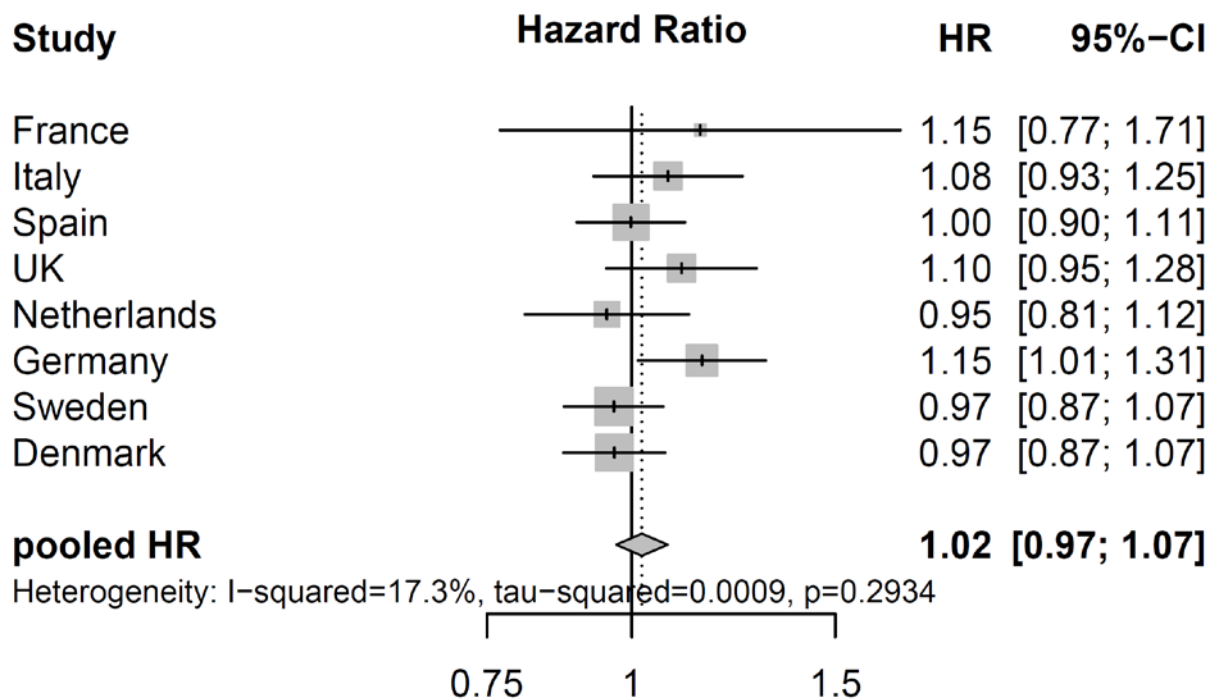
Mediators (continuous)	β (SE)	<i>p</i>
BMI, kg/m ²	0.04 (0.06)	0.52
Waist circumference, cm	0.19 (0.19)	0.33
CRP, mg/l	-0.06 (0.06)	0.38
HDL cholesterol, mmol/l	0.0009 (0.007)	0.90
Total cholesterol, mmol/l	-0.03 (0.02)	0.12
Triglycerides, mmol/l	-0.002 (0.01)	0.91
HbA _{1c} , mmol/mol	0.08 (0.08)	0.31

β obtained from linear regression; estimates are per fetuin-A-increasing allele of the weighted genetic score, adjusted for country among 10,850 subcohort participants

Supplemental Table 4– Instrumental variable estimates for the weighted genetic score in strata of age, sex, waist circumference, and HbA_{1c} in the EPIC-InterAct study

Strata	HR (95% CI) per 50µg/ml increase in fetuin-A concentration
Age≤55 years (n=11,953)	1.01 (0.92, 1.11)
Age>55years (n=10,426)	1.04 (0.97, 1.10)
Men (n=9,691)	1.03 (0.93, 1.13)
Women (n=12,688)	1.03 (0.94, 1.11)
Low waist circumference (n=10,450) (Men: ≤98 cm, Women: ≤84 cm)	1.01 (0.93, 1.10)
High waist circumference (n=10,163) (Men: >98 cm, Women: >84 cm)	1.02 (0.96, 1.09)
HbA _{1c} ≤5.6% (38 mmol/mol) (n=12,064)	1.03 (0.93, 1.12)
HbA _{1c} >5.6% (38 mmol/mol) (n=9,865)	0.97 (0.89, 1.07)

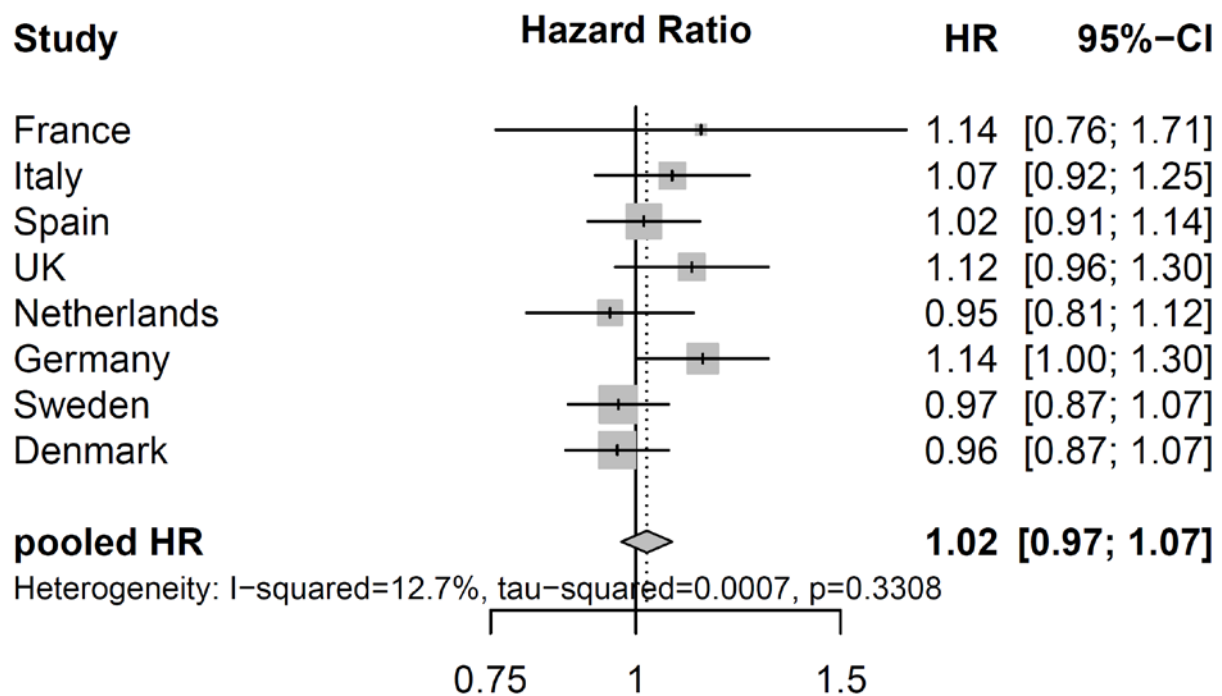
Instrumental variable estimates were obtained from two-stage least squares procedure. Data are adjusted for age, sex, study center, and genotyping source. Analyses have been performed stratified by country and combined with random-effects meta-analysis.



Supplemental Figure 1 – Forest plot of the association of the weighted genetic score with diabetes risk in the EPIC-InterAct study by country

Data are HRs and 95% CIs per fetuin-A-increasing allele, adjusted for age, sex, study center, and genotyping source. Analyses have been performed stratified by country and combined with random-effects meta-analysis.

$n=22,379$ including 12,975 incident cases of type 2 diabetes



Supplemental Figure 2 – Forest plot of the association of the unweighted genetic score with diabetes risk in the EPIC-InterAct study by country

Data are HRs and 95% CIs per fetuin-A-increasing allele, adjusted for age, sex, study center, and genotyping source. Analyses have been performed stratified by country and combined with random-effects meta-analysis.

n=22,379 including 12,975 incident cases of type 2 diabetes

